

SEQUENCE LISTING

<110> BASF Plant Science GmbH

<120> TER gene of Euglena

<130> AE 20030715

<140> PF 54922

<141> 2003-10-10

<160> 11

<170> PatentIn version 3.1

<210> 1

<211> 1620

<212> DNA

<213> Euglena gracilis

<220>

<221> CDS

<222> (1) .. (1620)

<223>

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2

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Gly	Val	Asp	Arg	Gly	Leu	Met	Arg	Pro	Thr	Thr	Ala	Ala	Ala	Leu	Thr	
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Ser	Val	Arg	Arg	Pro	Leu	Ala	Ala	Leu	Ala	Glu	Leu	Pro	Thr	Ala	Val	
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Gly	Cys	Glu	Lys	Arg	Val	Gln	Glu	Glu	Ile	Ala	Tyr	Ala	Arg	Ala	His	
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Pro	Pro	Thr	Ser	Pro	Gly	Pro	Lys	Arg	Val	Leu	Val	Ile	Gly	Cys	Ser	
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Leu	Glu	Ala	Gly	Leu	Tyr	Ala	Arg	Ser	Leu	Asn	Gly	Asp	Ala	Phe	Asp	
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Ser	Thr	Thr	Lys	Ala	Arg	Thr	Val	Glu	Ala	Ile	Lys	Arg	Asp	Leu	Gly	
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acg	gtg	gac	ctc	gtg	gtg	tac	agc	atc	gcc	gcc	ccg	aag	cgg	acg	gac	864
Thr	Val	Asp	Leu	Val	Val	Tyr	Ser	Ile	Ala	Ala	Pro	Lys	Arg	Thr	Asp	
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Val	Ser	Ile	Glu	Pro	Ala	Ser	Pro	Glu	Glu	Ile	Ala	Asp	Thr	Val	Lys	
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Gly	Cys	Pro	Ala	Tyr	Pro	Val	Val	Ala	Lys	Ala	Leu	Val	Thr	Gln	Ala	
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Ser	Ser	Ala	Ile	Pro	Val	Val	Pro	Leu	Tyr	Ile	Cys	Leu	Leu	Tyr	Arg	
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Val	Met	Lys	Glu	Lys	Gly	Thr	His	Glu	Gly	Cys	Ile	Glu	Gln	Met	Val	
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Arg	Leu	Leu	Thr	Thr	Lys	Leu	Tyr	Pro	Glu	Asn	Gly	Ala	Pro	Ile	Val	
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4

Asp Glu Ala Gly Arg Val Arg Val Asp Asp Trp Glu Met Ala Glu Asp
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 gtg cag cag gct gtt aag gac ctc tgg agc cag gtg agc act gcc aac 1488
 Val Gln Gln Ala Val Lys Asp Leu Trp Ser Gln Val Ser Thr Ala Asn
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 ctc aag gac atc tcc gac ttc gct ggg tat caa act gag ttc ctg cgg 1536
 Leu Lys Asp Ile Ser Asp Phe Ala Gly Tyr Gln Thr Glu Phe Leu Arg
 500 505 510
 ctg ttc ggg ttc ggc att gac ggc gtg gac tac gac cag ccc gtg gac 1584
 Leu Phe Gly Phe Gly Ile Asp Gly Val Asp Tyr Asp Gln Pro Val Asp
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 gtg gag gcg gac ctc ccc agt gct gcc cag cag tag 1620
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<211> 539

<212> PRT

<213> *Euglena gracilis*

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 35 40 45
 Gly Val Asp Arg Gly Leu Met Arg Pro Thr Thr Ala Ala Ala Leu Thr
 50 55 60
 Thr Met Arg Glu Val Pro Gln Met Ala Glu Gly Phe Ser Gly Glu Ala
 65 70 75 80
 Thr Ser Ala Trp Ala Ala Ala Gly Pro Gln Trp Ala Ala Pro Leu Val
 85 90 95

5

Ala Ala Ala Ser Ser Ala Leu Ala Leu Trp Trp Trp Ala Ala Arg Arg
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Ser Val Arg Arg Pro Leu Ala Ala Leu Ala Glu Leu Pro Thr Ala Val
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Thr His Leu Ala Pro Pro Met Ala Met Phe Thr Thr Thr Ala Lys Val
 130 135 140

Ile Gln Pro Lys Ile Arg Gly Phe Ile Cys Thr Thr Thr His Pro Ile
 145 150 155 160

Gly Cys Glu Lys Arg Val Gln Glu Glu Ile Ala Tyr Ala Arg Ala His
 165 170 175

Pro Pro Thr Ser Pro Gly Pro Lys Arg Val Leu Val Ile Gly Cys Ser
 180 185 190

Thr Gly Tyr Gly Leu Ser Thr Arg Ile Thr Ala Ala Phe Gly Tyr Gln
 195 200 205

Ala Ala Thr Leu Gly Val Phe Leu Ala Gly Pro Pro Thr Lys Gly Arg
 210 215 220

Pro Ala Ala Ala Gly Trp Tyr Asn Thr Val Ala Phe Glu Lys Ala Ala
 225 230 235 240

Leu Glu Ala Gly Leu Tyr Ala Arg Ser Leu Asn Gly Asp Ala Phe Asp
 245 250 255

Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly
 260 265 270

Thr Val Asp Leu Val Val Tyr Ser Ile Ala Ala Pro Lys Arg Thr Asp
 275 280 285

Pro Ala Thr Gly Val Leu His Lys Ala Cys Leu Lys Pro Ile Gly Ala
 290 295 300

Thr Tyr Thr Asn Arg Thr Val Asn Thr Asp Lys Ala Glu Val Thr Asp
 305 310 315 320

6

Val Ser Ile Glu Pro Ala Ser Pro Glu Glu Ile Ala Asp Thr Val Lys
 325 330 335

Val Met Gly Gly Glu Asp Trp Glu Leu Trp Ile Gln Ala Leu Ser Glu
 340 345 350

Ala Gly Val Leu Ala Glu Gly Ala Lys Thr Val Ala Tyr Ser Tyr Ile
 355 360 365

Gly Pro Glu Met Thr Trp Pro Val Tyr Trp Ser Gly Thr Ile Gly Glu
 370 375 380

Ala Lys Lys Asp Val Glu Lys Ala Ala Lys Arg Ile Thr Gln Gln Tyr
 385 390 395 400

Gly Cys Pro Ala Tyr Pro Val Val Ala Lys Ala Leu Val Thr Gln Ala
 405 410 415

Ser Ser Ala Ile Pro Val Val Pro Leu Tyr Ile Cys Leu Leu Tyr Arg
 420 425 430

Val Met Lys Glu Lys Gly Thr His Glu Gly Cys Ile Glu Gln Met Val
 435 440 445

Arg Leu Leu Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val
 450 455 460

Asp Glu Ala Gly Arg Val Arg Val Asp Asp Trp Glu Met Ala Glu Asp
 465 470 475 480

Val Gln Gln Ala Val Lys Asp Leu Trp Ser Gln Val Ser Thr Ala Asn
 485 490 495

Leu Lys Asp Ile Ser Asp Phe Ala Gly Tyr Gln Thr Glu Phe Leu Arg
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<212> DNA

<213> *Euglena gracilis*

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cgggatctcg gcacgggtgga cctcgtggtg tacagcatcg ccgccccgaa acggacggac      180
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gtggagaagg ccgctaagcg catcacacag cagtacggct gccagcata cccggtggtg      540
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ctgctgtacc gcgttatgaa ggagaagggc acccacgagg gctgcatcga gcagatggtg      660
cggctgctca ccacgaagct gtaccocggg aacggttccc ccattgtcga tgaggccggg      720
cgggtgcggg tggatgactg ggagatggcg gaggatgtgc agcaggctgt gaaggacctc      780
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<222> (1) .. (1329)

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ctc ctc cgc act ggc gct gtg gtg gtg aac atc gcc acc gcg gtc acc	96
Leu Leu Arg Thr Gly Ala Val Val Val Asn Ile Ala Thr Ala Val Thr	
20 25 30	
cac ctg gcc ccc ccg atg gcg atg ttc acc acc aca gcg aag gtc atc	144
His Leu Ala Pro Pro Met Ala Met Phe Thr Thr Thr His Lys Val Ile	
35 40 45	
cag ccc aag att cgt ggc ttc atc tgc acg acc acc cac ccg atc ggc	192
Gln Pro Lys Ile Arg Gly Phe Ile Cys Thr Thr Thr His Pro Ile Gly	
50 55 60	
tgt gag aag cgg gtc cag gag gag atc gcg tac gcc cgt gcc cac ccg	240
Cys Glu Lys Arg Val Gln Glu Glu Ile Ala Tyr Ala Arg Ala His Pro	
65 70 75 80	
ccc acc agc cct ggc ccg aag agg gtg ctg gtc atc ggc tgc agt acc	288
Pro Thr Ser Pro Gly Pro Lys Arg Val Leu Val Ile Gly Cys Ser Thr	
85 90 95	
ggc tac ggg ctc tcc acc cgc atc acc gct gcc ttc ggc tac cag gcc	336
Gly Tyr Gly Leu Ser Thr Arg Ile Thr Ala Ala Phe Gly Tyr Gln Ala	
100 105 110	
gcc acg ctg ggc gtg ttc ctg gcg ggc ccc ccg acg aag ggc cgc ccc	384
Ala Thr Leu Gly Val Phe Leu Ala Gly Pro Pro Thr Lys Gly Arg Pro	
115 120 125	
gcc gcg gcg ggc tgg tac aac acc gtg gcg ttc gag aag gcc gcc ctg	432
Ala Ala Ala Gly Trp Tyr Asn Thr Val Ala Phe Glu Lys Ala Ala Leu	
130 135 140	
gag gcc ggg ctg tac gcc cgg agc ctt aat ggc gac gcc ttc gac tcc	480
Glu Ala Gly Leu Tyr Ala Arg Ser Leu Asn Gly Asp Ala Phe Asp Ser	
145 150 155 160	
aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc acg	528
Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly Thr	
165 170 175	
gtg gac ctc gtg gtg tac agc atc gcc gcc ccg aag cgg acg gac cct	576
Val Asp Leu Val Val Tyr Ser Ile Ala Ala Pro Lys Arg Thr Asp Pro	
180 185 190	
gcc acc ggc gtc ctc cac aag gcc tgc ctg aag ccc atc ggc gcc acg	624
Ala Thr Gly Val Leu His Lys Ala Cys Leu Lys Pro Ile Gly Ala Thr	
195 200 205	

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atg ggc ggg gag gac tgg gag ctc tgg atc cag gcg ctg tcg gag gcc Met Gly Gly Glu Ala Asp Trp Glu Leu Trp Ile Gln Ala Leu Ser Glu Ala 245 250 255	768
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ccc gag atg acg tgg cct gtc tac tgg tcc ggc acc atc ggg gag gcc Pro Glu Met Thr Trp Pro Val Tyr Trp Ser Gly Thr Ile Gly Glu Ala 275 280 285	864
aag aag gac gtg gag aag gct gcc aag cgc atc acg cag cag tac ggc Lys Lys Asp Val Glu Lys Ala Ala Lys Arg Ile Thr Gln Gln Tyr Gly 290 295 300	912
tgc ccg gcg tac ccg gtg gtg gcc aag gcc ttg gtc acc cag gcc agc Cys Pro Ala Tyr Pro Val Val Ala Lys Ala Leu Val Thr Gln Ala Ser 305 310 315 320	960
tcc gcc atc ccg gtg gtg ccg ctc tac atc tgc ctg ctg tac cgc gtt Ser Ala Ile Pro Val Val Pro Leu Tyr Ile Cys Leu Leu Tyr Arg Val 325 330 335	1008
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ctg ctc acc acg aag ctg tac ccc gag aac ggg gcc ccc atc gtc gat Leu Leu Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val Asp 355 360 365	1104
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aag gac atc tcc gac ttc gct ggg tat caa act gag ttc ctg cgg ctg Lys Asp Ile Ser Asp Phe Ala Gly Tyr Gln Thr Glu Phe Leu Arg Leu 405 410 415	1248
ttc ggg ttc ggc att gac ggc gtg gac tac gac cag ccc gtg gac gtg Phe Gly Phe Gly Ile Asp Gly Val Asp Tyr Asp Gln Pro Val Asp Val 420 425 430	1296

10

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1329

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<213> *Euglena gracilis*

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His Leu Ala Pro Pro Met Ala Met Phe Thr Thr Thr Ala Lys Val Ile
 35 40 45

Gln Pro Lys Ile Arg Gly Phe Ile Cys Thr Thr Thr His Pro Ile Gly
 50 55 60

Cys Glu Lys Arg Val Gln Glu Glu Ile Ala Tyr Ala Arg Ala His Pro
 65 70 75 80

Pro Thr Ser Pro Gly Pro Lys Arg Val Leu Val Ile Gly Cys Ser Thr
 85 90 95

Gly Tyr Gly Leu Ser Thr Arg Ile Thr Ala Ala Phe Gly Tyr Gln Ala
 100 105 110

Ala Thr Leu Gly Val Phe Leu Ala Gly Pro Pro Thr Lys Gly Arg Pro
 115 120 125

Ala Ala Ala Gly Trp Tyr Asn Thr Val Ala Phe Glu Lys Ala Ala Leu
 130 135 140

Glu Ala Gly Leu Tyr Ala Arg Ser Leu Asn Gly Asp Ala Phe Asp Ser
 145 150 155 160

Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly Thr
 165 170 175

Val Asp Leu Val Val Tyr Ser Ile Ala Ala Pro Lys Arg Thr Asp Pro
 180 185 190

Ala Thr Gly Val Leu His Lys Ala Cys Leu Lys Pro Ile Gly Ala Thr
 195 200 205

Tyr Thr Asn Arg Thr Val Asn Thr Asp Lys Ala Glu Val Thr Asp Val
 210 215 220

Ser Ile Glu Pro Ala Ser Pro Glu Glu Ile Ala Asp Thr Val Lys Val
 225 230 235 240

Met Gly Gly Glu Asp Trp Glu Leu Trp Ile Gln Ala Leu Ser Glu Ala
 245 250 255

Gly Val Leu Ala Glu Gly Ala Lys Thr Val Ala Tyr Ser Tyr Ile Gly
 260 265 270

Pro Glu Met Thr Trp Pro Val Tyr Trp Ser Gly Thr Ile Gly Glu Ala
 275 280 285

Lys Lys Asp Val Glu Lys Ala Ala Lys Arg Ile Thr Gln Gln Tyr Gly
 290 295 300

Cys Pro Ala Tyr Pro Val Val Ala Lys Ala Leu Val Thr Gln Ala Ser
 305 310 315 320

Ser Ala Ile Pro Val Val Pro Leu Tyr Ile Cys Leu Leu Tyr Arg Val
 325 330 335

Met Lys Glu Lys Gly Thr His Glu Gly Cys Ile Glu Gln Met Val Arg
 340 345 350

Leu Leu Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val Asp
 355 360 365

Glu Ala Gly Arg Val Arg Val Asp Asp Trp Glu Met Ala Glu Asp Val
 370 380

Gln Gln Ala Val Lys Asp Leu Trp Ser Gln Val Ser Thr Ala Asn Leu
 385 390 395 400

Lys Asp Ile Ser Asp Phe Ala Gly Tyr Gln Thr Glu Phe Leu Arg Leu
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<212> DNA

<213> *Euglena gracilis*

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<221> CDS

<222> (1)..(1212)

<223>

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 Ile Cys Thr Thr Thr His Pro Ile Gly Cys Glu Lys Arg Val Gln Glu
 20 25 30

gag atc gcg tac gcc cgt gcc cac ccg ccc acc agc cct ggc ccg aag 144
 Glu Ile Ala Tyr Ala Arg Ala His Pro Pro Thr Ser Pro Gly Pro Lys
 35 40 45

agg gtg ctg gtc atc ggc tgc agt acc ggc tac ggg ctc tcc acc cgc 192
 Arg Val Leu Val Ile Gly Cys Ser Thr Gly Tyr Gly Leu Ser Thr Arg
 50 55 60

atc acc gct gcc ttc ggc tac cag gcc gcc acg ctg ggc gtg ttc ctg 240

13

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Ala	Gly	Pro	Pro	Thr	Lys	Gly	Arg	Pro	Ala	Ala	Ala	Gly	Trp	Tyr	Asn	
				85				90						95		
acc	gtg	gcg	ttc	gag	aag	gcc	gcc	ctg	gag	gcc	ggg	ctg	tac	gcc	cgg	336
Thr	Val	Ala	Phe	Glu	Lys	Ala	Ala	Leu	Glu	Ala	Gly	Leu	Tyr	Ala	Arg	
			100					105					110			
agc	ctt	aat	ggc	gac	gcc	ttc	gac	tcc	aca	acg	aag	gcg	cgg	acg	gtc	384
Ser	Leu	Asn	Gly	Asp	Ala	Phe	Asp	Ser	Thr	Thr	Lys	Ala	Arg	Thr	Val	
		115					120					125				
gag	gcg	atc	aag	cgg	gac	ctc	ggc	acg	gtg	gac	ctc	gtg	gtg	tac	agc	432
Glu	Ala	Ile	Lys	Arg	Asp	Leu	Gly	Thr	Val	Asp	Leu	Val	Val	Tyr	Ser	
	130					135					140					
atc	gcc	gcc	ccg	aag	cgg	acg	gac	cct	gcc	acc	ggc	gtc	ctc	cac	aag	480
Ile	Ala	Ala	Pro	Lys	Arg	Thr	Asp	Pro	Ala	Thr	Gly	Val	Leu	His	Lys	
145					150					155					160	
gcc	tgc	ctg	aag	ccc	atc	ggc	gcc	acg	tac	acc	aac	cgc	act	gtg	aac	528
Ala	Cys	Leu	Lys	Pro	Ile	Gly	Ala	Thr	Tyr	Thr	Asn	Arg	Thr	Val	Asn	
				165				170					175			
acc	gac	aag	gcg	gag	gtg	acc	gac	gtc	agc	att	gag	ccg	gcc	tcc	ccc	576
Thr	Asp	Lys	Ala	Glu	Val	Thr	Asp	Val	Ser	Ile	Glu	Pro	Ala	Ser	Pro	
			180					185					190			
gaa	gag	atc	gcg	gac	acg	gtg	aag	gtg	atg	ggc	ggg	gag	gac	tgg	gag	624
Glu	Glu	Ile	Ala	Asp	Thr	Val	Lys	Val	Met	Gly	Gly	Glu	Asp	Trp	Glu	
		195					200					205				
ctc	tgg	atc	cag	gcg	ctg	tcg	gag	gcc	ggc	gtg	ctg	gcg	gag	ggg	gcc	672
Leu	Trp	Ile	Gln	Ala	Leu	Ser	Glu	Ala	Gly	Val	Leu	Ala	Glu	Gly	Ala	
	210					215					220					
aag	acg	gtg	gcg	tac	tcc	tac	atc	ggc	ccc	gag	atg	acg	tgg	cct	gtc	720
Lys	Thr	Val	Ala	Tyr	Ser	Tyr	Ile	Gly	Pro	Glu	Met	Thr	Trp	Pro	Val	
225					230					235				240		
tac	tgg	tcc	ggc	acc	atc	ggg	gag	gcc	aag	aag	gac	gtg	gag	aag	gct	768
Tyr	Trp	Ser	Gly	Thr	Ile	Gly	Glu	Ala	Lys	Lys	Asp	Val	Glu	Lys	Ala	
				245				250						255		
gcc	aag	cgc	atc	acg	cag	cag	tac	ggc	tgc	ccg	gcg	tac	ccg	gtg	gtg	816
Ala	Lys	Arg	Ile	Thr	Gln	Gln	Tyr	Gly	Cys	Pro	Ala	Tyr	Pro	Val	Val	
			260					265					270			
gcc	aag	gcc	ttg	gtc	acc	cag	gcc	agc	tcc	gcc	atc	ccg	gtg	gtg	ccg	864
Ala	Lys	Ala	Leu	Val	Thr	Gln	Ala	Ser	Ser	Ala	Ile	Pro	Val	Val	Pro	
		275					280					285				
ctc	tac	atc	tgc	ctg	ctg	tac	cgc	gtt	atg	aag	gag	aag	ggc	acc	cac	912

14

Leu Tyr Ile Cys Leu Leu Tyr Arg Val Met Lys Glu Lys Gly Thr His
 290 295 300
 gag ggc tgc atc gag cag atg gtg cgg ctg ctc acc acg aag ctg tac 960
 Glu Gly Cys Ile Glu Gln Met Val Arg Leu Leu Thr Thr Lys Leu Tyr
 305 310 315 320
 ccc gag aac ggg gcc ccc atc gtc gat gag gcc gga cgt gtg cgg gtg 1008
 Pro Glu Asn Gly Ala Pro Ile Val Asp Glu Ala Gly Arg Val Arg Val
 325 330 335
 gat gac tgg gag atg gcg gag gat gtg cag cag gct gtt aag gac ctc 1056
 Asp Asp Trp Glu Met Ala Glu Asp Val Gln Gln Ala Val Lys Asp Leu
 340 345 350
 tgg agc cag gtg agc act gcc aac ctc aag gac atc tcc gac ttc gct 1104
 Trp Ser Gln Val Ser Thr Ala Asn Leu Lys Asp Ile Ser Asp Phe Ala
 355 360 365
 ggg tat caa act gag ttc ctg cgg ctg ttc ggg ttc ggc att gac ggc 1152
 Gly Tyr Gln Thr Glu Phe Leu Arg Leu Phe Gly Phe Gly Ile Asp Gly
 370 375 380
 gtg gac tac gac cag ccc gtg gac gtg gag gcg gac ctc ccc agt gct 1200
 Val Asp Tyr Asp Gln Pro Val Asp Val Glu Ala Asp Leu Pro Ser Ala
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 Ala Gln Gln

<210> 7

<211> 403

<212> PRT

<213> *Euglena gracilis*

<400> 7

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 Ile Cys Thr Thr Thr His Pro Ile Gly Cys Glu Lys Arg Val Gln Glu
 20 25 30
 Glu Ile Ala Tyr Ala Arg Ala His Pro Pro Thr Ser Pro Gly Pro Lys
 35 40 45

15

Arg	Val	Leu	Val	Ile	Gly	Cys	Ser	Thr	Gly	Tyr	Gly	Leu	Ser	Thr	Arg
50						55					60				
Ile	Thr	Ala	Ala	Phe	Gly	Tyr	Gln	Ala	Ala	Thr	Leu	Gly	Val	Phe	Leu
65					70					75					80
Ala	Gly	Pro	Pro	Thr	Lys	Gly	Arg	Pro	Ala	Ala	Ala	Gly	Trp	Tyr	Asn
				85					90					95	
Thr	Val	Ala	Phe	Glu	Lys	Ala	Ala	Leu	Glu	Ala	Gly	Leu	Tyr	Ala	Arg
		100						105					110		
Ser	Leu	Asn	Gly	Asp	Ala	Phe	Asp	Ser	Thr	Thr	Lys	Ala	Arg	Thr	Val
		115						120					125		
Glu	Ala	Ile	Lys	Arg	Asp	Leu	Gly	Thr	Val	Asp	Leu	Val	Val	Tyr	Ser
130						135					140				
Ile	Ala	Ala	Pro	Lys	Arg	Thr	Asp	Pro	Ala	Thr	Gly	Val	Leu	His	Lys
145					150					155					160
Ala	Cys	Leu	Lys	Pro	Ile	Gly	Ala	Thr	Tyr	Thr	Asn	Arg	Thr	Val	Asn
				165					170					175	
Thr	Asp	Lys	Ala	Glu	Val	Thr	Asp	Val	Ser	Ile	Glu	Pro	Ala	Ser	Pro
			180					185					190		
Glu	Glu	Ile	Ala	Asp	Thr	Val	Lys	Val	Met	Gly	Gly	Glu	Asp	Trp	Glu
		195						200				205			
Leu	Trp	Ile	Gln	Ala	Leu	Ser	Glu	Ala	Gly	Val	Leu	Ala	Glu	Gly	Ala
210						215					220				
Lys	Thr	Val	Ala	Tyr	Ser	Tyr	Ile	Gly	Pro	Glu	Met	Thr	Trp	Pro	Val
225					230					235				240	
Tyr	Trp	Ser	Gly	Thr	Ile	Gly	Glu	Ala	Lys	Lys	Asp	Val	Glu	Lys	Ala
			245						250					255	
Ala	Lys	Arg	Ile	Thr	Gln	Gln	Tyr	Gly	Cys	Pro	Ala	Tyr	Pro	Val	Val
			260					265					270		

16

Ala Lys Ala Leu Val Thr Gln Ala Ser Ser Ala Ile Pro Val Val Pro
 275 280 285

Leu Tyr Ile Cys Leu Leu Tyr Arg Val Met Lys Glu Lys Gly Thr His
 290 295 300

Glu Gly Cys Ile Glu Gln Met Val Arg Leu Leu Thr Thr Lys Leu Tyr
 305 310 315 320

Pro Glu Asn Gly Ala Pro Ile Val Asp Glu Ala Gly Arg Val Arg Val
 325 330 335

Asp Asp Trp Glu Met Ala Glu Asp Val Gln Gln Ala Val Lys Asp Leu
 340 345 350

Trp Ser Gln Val Ser Thr Ala Asn Leu Lys Asp Ile Ser Asp Phe Ala
 355 360 365

Gly Tyr Gln Thr Glu Phe Leu Arg Leu Phe Gly Phe Gly Ile Asp Gly
 370 375 380

Val Asp Tyr Asp Gln Pro Val Asp Val Glu Ala Asp Leu Pro Ser Ala
 385 390 395 400

Ala Gln Gln

<210> 8

<211> 1803

<212> DNA

<213> *Euglena gracilis*

<220>

<221> CDS

<222> (1) .. (1803)

<223>

17

<400> 8

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Met Ala Ser Met Ile Ser Ser Ser Ala Val Thr Thr Val Ser Arg Ala	
1 5 10 15	
tct acg gtg caa tcg gcc gcg gtg gct cca ttc ggc ggc ctc aaa tcc	96
Ser Thr Val Gln Ser Ala Ala Val Ala Pro Phe Gly Gly Leu Lys Ser	
20 25 30	
atg act gga ttc cca gtt aag aag gtc aac act gac att act tcc att	144
Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile	
35 40 45	
aca agc aat ggt gga aga gta aag tat tta aat ctc gag atg tcg tgc	192
Thr Ser Asn Gly Gly Arg Val Lys Tyr Leu Asn Leu Glu Met Ser Cys	
50 55 60	
ccc gcc tcg ccg tct gct gcc gtg gtg tct gcc ggc gcc ctc tgc ctg	240
Pro Ala Ser Pro Ser Ala Ala Val Val Ser Ala Gly Ala Leu Cys Leu	
65 70 75 80	
tgc gtg gca acg gta ttg ttg gcg act gga tcc aac ccc acc gcc ctg	288
Cys Val Ala Thr Val Leu Leu Ala Thr Gly Ser Asn Pro Thr Ala Leu	
85 90 95	
tcc act gct tcc act cgc tct ccg acc tca ctg gtc cgt ggg gtg gac	336
Ser Thr Ala Ser Thr Arg Ser Pro Thr Ser Leu Val Arg Gly Val Asp	
100 105 110	
agg ggc ttg atg agg cca acc act gca gcg gct ctg acg aca atg aga	384
Arg Gly Leu Met Arg Pro Thr Thr Ala Ala Ala Leu Thr Thr Met Arg	
115 120 125	
gag gtg ccc cag atg gct gag gga ttt tca ggc gaa gcc acg tct gca	432
Glu Val Pro Gln Met Ala Glu Gly Phe Ser Gly Glu Ala Thr Ser Ala	
130 135 140	
tgg gcc gcc gcg ggg ccg cag tgg gcg gcg ccg ctc gtg gcc gcg gcc	480
Trp Ala Ala Ala Gly Pro Gln Trp Ala Ala Pro Leu Val Ala Ala Ala	
145 150 155 160	
tcc tcc gca ctg gcg ctg tgg tgg tgg gcc gcc ccg cgc agc gtg cgg	528
Ser Ser Ala Leu Ala Leu Trp Trp Trp Ala Ala Arg Arg Ser Val Arg	
165 170 175	
cgg ccg ctg gca gcg ctg gcg gag ctg ccc acc gcg gtc acc cac ctg	576
Arg Pro Leu Ala Ala Leu Ala Glu Leu Pro Thr Ala Val Thr His Leu	
180 185 190	
gcc ccc ccg atg gcg atg ttc acc acc aca gcg aag gtc atc cag ccc	624
Ala Pro Pro Met Ala Met Phe Thr Thr Thr Ala Lys Val Ile Gln Pro	
195 200 205	
aag att cgt ggc ttc atc tgc acg acc acc cac ccg atc ggc tgt gag	672
Lys Ile Arg Gly Phe Ile Cys Thr Thr Thr His Pro Ile Gly Cys Glu	
210 215 220	

aag cgg gtc cag gag gag atc gcg tac gcc cgt gcc cac ccg ccc acc	720
Lys Arg Val Gln Glu Glu Ile Ala Tyr Ala Arg Ala His Pro Pro Thr	
225 230 235 240	
agc cct ggc ccg aag agg gtg ctg gtc atc ggc tgc agt acc ggc tac	768
Ser Pro Gly Pro Lys Arg Val Leu Val Ile Gly Cys Ser Thr Gly Tyr	
245 250 255	
ggg ctc tcc acc cgc atc acc gct gcc ttc ggc tac cag gcc gcc acg	816
Gly Leu Ser Thr Arg Ile Thr Ala Ala Phe Gly Tyr Gln Ala Ala Thr	
260 265 270	
ctg ggc gtg ttc ctg gcg ggc ccc ccg acg aag ggc cgc ccc gcc gcg	864
Leu Gly Val Phe Leu Ala Gly Pro Pro Thr Lys Gly Arg Pro Ala Ala	
275 280 285	
gcg ggc tgg tac aac acc gtg gcg ttc gag aag gcc gcc ctg gag gcc	912
Ala Gly Trp Tyr Asn Thr Val Ala Phe Glu Lys Ala Ala Leu Glu Ala	
290 295 300	
ggg ctg tac gcc cgg agc ctt aat ggc gac gcc ttc gac tcc aca acg	960
Gly Leu Tyr Ala Arg Ser Leu Asn Gly Asp Ala Phe Asp Ser Thr Thr	
305 310 315 320	
aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc acg gtg gac	1008
Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly Thr Val Asp	
325 330 335	
ctc gtg gtg tac agc atc gcc gcc ccg aag cgg acg gac cct gcc acc	1056
Leu Val Val Tyr Ser Ile Ala Ala Pro Lys Arg Thr Asp Pro Ala Thr	
340 345 350	
ggc gtc ctc cac aag gcc tgc ctg aag ccc atc ggc gcc acg tac acc	1104
Gly Val Leu His Lys Ala Cys Leu Lys Pro Ile Gly Ala Thr Tyr Thr	
355 360 365	
aac cgc act gtg aac acc gac aag gcg gag gtg acc gac gtc agc att	1152
Asn Arg Thr Val Asn Thr Asp Lys Ala Glu Val Thr Asp Val Ser Ile	
370 375 380	
gag ccg gcc tcc ccc gaa gag atc gcg gac acg gtg aag gtg atg ggc	1200
Glu Pro Ala Ser Pro Glu Glu Ile Ala Asp Thr Val Lys Val Met Gly	
385 390 395 400	
ggg gag gac tgg gag ctc tgg atc cag gcg ctg tcg gag gcc ggc gtg	1248
Gly Glu Asp Trp Glu Leu Trp Ile Gln Ala Leu Ser Glu Ala Gly Val	
405 410 415	
ctg gcg gag ggg gcc aag acg gtg gcg tac tcc tac atc ggc ccc gag	1296
Leu Ala Glu Gly Ala Lys Thr Val Ala Tyr Ser Tyr Ile Gly Pro Glu	
420 425 430	
atg acg tgg cct gtc tac tgg tcc ggc acc atc ggg gag gcc aag aag	1344
Met Thr Trp Pro Val Tyr Trp Ser Gly Thr Ile Gly Glu Ala Lys Lys	
435 440 445	

19

gac gtg gag aag gct gcc aag cgc atc acg cag cag tac ggc tgc ccg 1392
 Asp Val Glu Lys Ala Ala Lys Arg Ile Thr Gln Gln Tyr Gly Cys Pro
 450 455 460

gcg tac ccg gtg gtg gcc aag gcc ttg gtc acc cag gcc agc tcc gcc 1440
 Ala Tyr Pro Val Val Ala Lys Ala Leu Val Thr Gln Ala Ser Ser Ala
 465 470 475 480

atc ccg gtg gtg ccg ctc tac atc tgc ctg ctg tac cgc gtt atg aag 1488
 Ile Pro Val Val Pro Leu Tyr Ile Cys Leu Leu Tyr Arg Val Met Lys
 485 490 495

gag aag ggc acc cac gag ggc tgc atc gag cag atg gtg cgg ctg ctc 1536
 Glu Lys Gly Thr His Glu Gly Cys Ile Glu Gln Met Val Arg Leu Leu
 500 505 510

acc acg aag ctg tac ccc gag aac ggg gcc ccc atc gtc gat gag gcc 1584
 Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val Asp Glu Ala
 515 520 525

gga cgt gtg cgg gtg gat gac tgg gag atg gcg gag gat gtg cag cag 1632
 Gly Arg Val Arg Val Asp Asp Trp Glu Met Ala Glu Asp Val Gln Gln
 530 535 540

gct gtt aag gac ctc tgg agc cag gtg agc act gcc aac ctc aag gac 1680
 Ala Val Lys Asp Leu Trp Ser Gln Val Ser Thr Ala Asn Leu Lys Asp
 545 550 555 560

atc tcc gac ttc gct ggg tat caa act gag ttc ctg cgg ctg ttc ggg 1728
 Ile Ser Asp Phe Ala Gly Tyr Gln Thr Glu Phe Leu Arg Leu Phe Gly
 565 570 575

ttc ggc att gac ggc gtg gac tac gac cag ccc gtg gac gtg gag gcg 1776
 Phe Gly Ile Asp Gly Val Asp Tyr Asp Gln Pro Val Asp Val Glu Ala
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gac ctc ccc agt gct gcc cag cag tag 1803
 Asp Leu Pro Ser Ala Ala Gln Gln
 595 600

<210> 9

<211> 600

<212> PRT

<213> Euglena gracilis

<400> 9

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Ser Thr Val Gln Ser Ala Ala Val Ala Pro Phe Gly Gly Leu Lys Ser
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Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Tyr Leu Asn Leu Glu Met Ser Cys
50 55 60

Pro Ala Ser Pro Ser Ala Ala Val Val Ser Ala Gly Ala Leu Cys Leu
65 70 75 80

Cys Val Ala Thr Val Leu Leu Ala Thr Gly Ser Asn Pro Thr Ala Leu
85 90 95

Ser Thr Ala Ser Thr Arg Ser Pro Thr Ser Leu Val Arg Gly Val Asp
100 105 110

Arg Gly Leu Met Arg Pro Thr Thr Ala Ala Ala Leu Thr Thr Met Arg
115 120 125

Glu Val Pro Gln Met Ala Glu Gly Phe Ser Gly Glu Ala Thr Ser Ala
130 135 140

Trp Ala Ala Ala Gly Pro Gln Trp Ala Ala Pro Leu Val Ala Ala Ala
145 150 155 160

Ser Ser Ala Leu Ala Leu Trp Trp Trp Ala Ala Arg Arg Ser Val Arg
165 170 175

Arg Pro Leu Ala Ala Leu Ala Glu Leu Pro Thr Ala Val Thr His Leu
180 185 190

Ala Pro Pro Met Ala Met Phe Thr Thr Thr Ala Lys Val Ile Gln Pro
195 200 205

Lys Ile Arg Gly Phe Ile Cys Thr Thr Thr His Pro Ile Gly Cys Glu
210 215 220

Lys Arg Val Gln Glu Glu Ile Ala Tyr Ala Arg Ala His Pro Pro Thr
225 230 235 240

Ser Pro Gly Pro Lys Arg Val Leu Val Ile Gly Cys Ser Thr Gly Tyr
 245 250 255

Gly Leu Ser Thr Arg Ile Thr Ala Ala Phe Gly Tyr Gln Ala Ala Thr
 260 265 270

Leu Gly Val Phe Leu Ala Gly Pro Pro Thr Lys Gly Arg Pro Ala Ala
 275 280 285

Ala Gly Trp Tyr Asn Thr Val Ala Phe Glu Lys Ala Ala Leu Glu Ala
 290 295 300

Gly Leu Tyr Ala Arg Ser Leu Asn Gly Asp Ala Phe Asp Ser Thr Thr
 305 310 315 320

Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly Thr Val Asp
 325 330 335

Leu Val Val Tyr Ser Ile Ala Ala Pro Lys Arg Thr Asp Pro Ala Thr
 340 345 350

Gly Val Leu His Lys Ala Cys Leu Lys Pro Ile Gly Ala Thr Tyr Thr
 355 360 365

Asn Arg Thr Val Asn Thr Asp Lys Ala Glu Val Thr Asp Val Ser Ile
 370 375 380

Glu Pro Ala Ser Pro Glu Glu Ile Ala Asp Thr Val Lys Val Met Gly
 385 390 395 400

Gly Glu Asp Trp Glu Leu Trp Ile Gln Ala Leu Ser Glu Ala Gly Val
 405 410 415

Leu Ala Glu Gly Ala Lys Thr Val Ala Tyr Ser Tyr Ile Gly Pro Glu
 420 425 430

Met Thr Trp Pro Val Tyr Trp Ser Gly Thr Ile Gly Glu Ala Lys Lys
 435 440 445

Asp Val Glu Lys Ala Ala Lys Arg Ile Thr Gln Gln Tyr Gly Cys Pro
 450 455 460

Ala Tyr Pro Val Val Ala Lys Ala Leu Val Thr Gln Ala Ser Ser Ala
 465 470 475 480

Ile Pro Val Val Pro Leu Tyr Ile Cys Leu Leu Tyr Arg Val Met Lys
 485 490 495

Glu Lys Gly Thr His Glu Gly Cys Ile Glu Gln Met Val Arg Leu Leu
 500 505 510

Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val Asp Glu Ala
 515 520 525

Gly Arg Val Arg Val Asp Asp Trp Glu Met Ala Glu Asp Val Gln Gln
 530 535 540

Ala Val Lys Asp Leu Trp Ser Gln Val Ser Thr Ala Asn Leu Lys Asp
 545 550 555 560

Ile Ser Asp Phe Ala Gly Tyr Gln Thr Glu Phe Leu Arg Leu Phe Gly
 565 570 575

Phe Gly Ile Asp Gly Val Asp Tyr Asp Gln Pro Val Asp Val Glu Ala
 580 585 590

Asp Leu Pro Ser Ala Ala Gln Gln
 595 600

<210> 10

<211> 1389

<212> DNA

<213> *Euglena gracilis*

<220>

<221> CDS

<222> (1) .. (1389)

<223>

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tct acg gtg caa tcg gcc gcg gtg gct cca ttc ggc ggc ctc aaa tcc 96
 Ser Thr Val Gln Ser Ala Ala Val Ala Pro Phe Gly Gly Leu Lys Ser
 20 25 30

atg act gga ttc cca gtt aag aag gtc aac act gac att act tcc att 144
 Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
 35 40 45

aca agc aat ggt gga aga gta aag tat tta aat atg ttc acc acc aca 192
 Thr Ser Asn Gly Gly Arg Val Lys Tyr Leu Asn Met Phe Thr Thr Thr
 50 55 60

gcg aag gtc atc cag ccc aag att cgt ggc ttc atc tgc acg acc acc 240
 Ala Lys Val Ile Gln Pro Lys Ile Arg Gly Phe Ile Cys Thr Thr Thr
 65 70 75 80

cac ccg atc ggc tgt gag aag cgg gtc cag gag gag atc gcg tac gcc 288
 His Pro Ile Gly Cys Glu Lys Arg Val Gln Glu Glu Ile Ala Tyr Ala
 85 90 95

cgt gcc cac ccg ccc acc agc cct ggc ccg aag agg gtg ctg gtc atc 336
 Arg Ala His Pro Pro Thr Ser Pro Gly Pro Lys Arg Val Leu Val Ile
 100 105 110

ggc tgc agt acc ggc tac ggg ctc tcc acc cgc atc acc gct gcc ttc 384
 Gly Cys Ser Thr Gly Tyr Gly Leu Ser Thr Arg Ile Thr Ala Ala Phe
 115 120 125

ggc tac cag gcc gcc acg ctg ggc gtg ttc ctg gcg ggc ccc ccg acg 432
 Gly Tyr Gln Ala Ala Thr Leu Gly Val Phe Leu Ala Gly Pro Pro Thr
 130 135 140

aag ggc cgc ccc gcc gcg gcg ggc tgg tac aac acc gtg gcg ttc gag 480
 Lys Gly Arg Pro Ala Ala Ala Gly Trp Tyr Asn Thr Val Ala Phe Glu
 145 150 155 160

aag gcc gcc ctg gag gcc ggg ctg tac gcc cgg agc ctt aat ggc gac 528
 Lys Ala Ala Leu Glu Ala Gly Leu Tyr Ala Arg Ser Leu Asn Gly Asp
 165 170 175

gcc ttc gac tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg 576
 Ala Phe Asp Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg
 180 185 190

gac ctc ggc acg gtg gac ctc gtg gtg tac agc atc gcc gcc ccg aag 624
 Asp Leu Gly Thr Val Asp Leu Val Val Tyr Ser Ile Ala Ala Pro Lys
 195 200 205

cgg acg gac cct gcc acc ggc gtc ctc cac aag gcc tgc ctg aag ccc 672

24

Arg	Thr	Asp	Pro	Ala	Thr	Gly	Val	Leu	His	Lys	Ala	Cys	Leu	Lys	Pro	
210						215					220					
atc	ggc	gcc	acg	tac	acc	aac	cgc	act	gtg	aac	acc	gac	aag	gcg	gag	720
Ile	Gly	Ala	Thr	Tyr	Thr	Asn	Arg	Thr	Val	Asn	Thr	Asp	Lys	Ala	Glu	
225					230					235					240	
gtg	acc	gac	gtc	agc	att	gag	ccg	gcc	tcc	ccc	gaa	gag	atc	gcg	gac	768
Val	Thr	Asp	Val	Ser	Ile	Glu	Pro	Ala	Ser	Pro	Glu	Glu	Ile	Ala	Asp	
				245					250						255	
acg	gtg	aag	gtg	atg	ggc	ggg	gag	gac	tgg	gag	ctc	tgg	atc	cag	gcg	816
Thr	Val	Lys	Val	Met	Gly	Gly	Glu	Asp	Trp	Glu	Leu	Trp	Ile	Gln	Ala	
			260					265						270		
ctg	tcg	gag	gcc	ggc	gtg	ctg	gcg	gag	ggg	gcc	aag	acg	gtg	gcg	tac	864
Leu	Ser	Glu	Ala	Gly	Val	Leu	Ala	Glu	Gly	Ala	Lys	Thr	Val	Ala	Tyr	
		275					280						285			
tcc	tac	atc	ggc	ccc	gag	atg	acg	tgg	cct	gtc	tac	tgg	tcc	ggc	acc	912
Ser	Tyr	Ile	Gly	Pro	Glu	Met	Thr	Trp	Pro	Val	Tyr	Trp	Ser	Gly	Thr	
	290					295					300					
atc	ggg	gag	gcc	aag	aag	gac	gtg	gag	aag	gct	gcc	aag	cgc	atc	acg	960
Ile	Gly	Glu	Ala	Lys	Lys	Asp	Val	Glu	Lys	Ala	Ala	Lys	Arg	Ile	Thr	
305					310					315					320	
cag	cag	tac	ggc	tgc	ccg	gcg	tac	ccg	gtg	gtg	gcc	aag	gcc	ttg	gtc	1008
Gln	Gln	Tyr	Gly	Cys	Pro	Ala	Tyr	Pro	Val	Val	Ala	Lys	Ala	Leu	Val	
				325					330					335		
acc	cag	gcc	agc	tcc	gcc	atc	ccg	gtg	gtg	ccg	ctc	tac	atc	tgc	ctg	1056
Thr	Gln	Ala	Ser	Ser	Ala	Ile	Pro	Val	Val	Pro	Leu	Tyr	Ile	Cys	Leu	
			340					345					350			
ctg	tac	cgc	gtt	atg	aag	gag	aag	ggc	acc	cac	gag	ggc	tgc	atc	gag	1104
Leu	Tyr	Arg	Val	Met	Lys	Glu	Lys	Gly	Thr	His	Glu	Gly	Cys	Ile	Glu	
		355					360					365				
cag	atg	gtg	cgg	ctg	ctc	acc	acg	aag	ctg	tac	ccc	gag	aac	ggg	gcc	1152
Gln	Met	Val	Arg	Leu	Leu	Thr	Thr	Lys	Leu	Tyr	Pro	Glu	Asn	Gly	Ala	
		370				375					380					
ccc	atc	gtc	gat	gag	gcc	gga	cgt	gtg	cgg	gtg	gat	gac	tgg	gag	atg	1200
Pro	Ile	Val	Asp	Glu	Ala	Gly	Arg	Val	Arg	Val	Asp	Asp	Trp	Glu	Met	
385					390					395					400	
gcg	gag	gat	gtg	cag	cag	gct	gtt	aag	gac	ctc	tgg	agc	cag	gtg	agc	1248
Ala	Glu	Asp	Val	Gln	Gln	Ala	Val	Lys	Asp	Leu	Trp	Ser	Gln	Val	Ser	
				405					410					415		
act	gcc	aac	ctc	aag	gac	atc	tcc	gac	ttc	gct	ggg	tat	caa	act	gag	1296
Thr	Ala	Asn	Leu	Lys	Asp	Ile	Ser	Asp	Phe	Ala	Gly	Tyr	Gln	Thr	Glu	
			420					425					430			
ttc	ctg	cgg	ctg	ttc	ggg	ttc	ggc	att	gac	ggc	gtg	gac	tac	gac	cag	1344

25

Phe Leu Arg Leu Phe Gly Phe Gly Ile Asp Gly Val Asp Tyr Asp Gln
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Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
 35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Tyr Leu Asn Met Phe Thr Thr Thr
 50 55 60

Ala Lys Val Ile Gln Pro Lys Ile Arg Gly Phe Ile Cys Thr Thr Thr
 65 70 75 80

His Pro Ile Gly Cys Glu Lys Arg Val Gln Glu Glu Ile Ala Tyr Ala
 85 90 95

Arg Ala His Pro Pro Thr Ser Pro Gly Pro Lys Arg Val Leu Val Ile
 100 105 110

Gly Cys Ser Thr Gly Tyr Gly Leu Ser Thr Arg Ile Thr Ala Ala Phe
 115 120 125

Gly Tyr Gln Ala Ala Thr Leu Gly Val Phe Leu Ala Gly Pro Pro Thr
 130 135 140

26

Lys Gly Arg Pro Ala Ala Ala Gly Trp Tyr Asn Thr Val Ala Phe Glu
 145 150 155 160

Lys Ala Ala Leu Glu Ala Gly Leu Tyr Ala Arg Ser Leu Asn Gly Asp
 165 170 175

Ala Phe Asp Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg
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Asp Leu Gly Thr Val Asp Leu Val Val Tyr Ser Ile Ala Ala Pro Lys
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Arg Thr Asp Pro Ala Thr Gly Val Leu His Lys Ala Cys Leu Lys Pro
 210 215 220

Ile Gly Ala Thr Tyr Thr Asn Arg Thr Val Asn Thr Asp Lys Ala Glu
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Val Thr Asp Val Ser Ile Glu Pro Ala Ser Pro Glu Glu Ile Ala Asp
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Thr Val Lys Val Met Gly Gly Glu Asp Trp Glu Leu Trp Ile Gln Ala
 260 265 270

Leu Ser Glu Ala Gly Val Leu Ala Glu Gly Ala Lys Thr Val Ala Tyr
 275 280 285

Ser Tyr Ile Gly Pro Glu Met Thr Trp Pro Val Tyr Trp Ser Gly Thr
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Ile Gly Glu Ala Lys Lys Asp Val Glu Lys Ala Ala Lys Arg Ile Thr
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Gln Gln Tyr Gly Cys Pro Ala Tyr Pro Val Val Ala Lys Ala Leu Val
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Thr Gln Ala Ser Ser Ala Ile Pro Val Val Pro Leu Tyr Ile Cys Leu
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Leu Tyr Arg Val Met Lys Glu Lys Gly Thr His Glu Gly Cys Ile Glu
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27

Gln Met Val Arg Leu Leu Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala
370 375 380

Pro Ile Val Asp Glu Ala Gly Arg Val Arg Val Asp Asp Trp Glu Met
385 390 395 400

Ala Glu Asp Val Gln Gln Ala Val Lys Asp Leu Trp Ser Gln Val Ser
405 410 415

Thr Ala Asn Leu Lys Asp Ile Ser Asp Phe Ala Gly Tyr Gln Thr Glu
420 425 430

Phe Leu Arg Leu Phe Gly Phe Gly Ile Asp Gly Val Asp Tyr Asp Gln
435 440 445

Pro Val Asp Val Glu Ala Asp Leu Pro Ser Ala Ala Gln Gln
450 455 460